



SEQUENCE LISTING

#7

SEQUENCE LISTING

<110> Shimkets, Richard A.  
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Li, Li  
Gorman, Linda  
Gusev, Vladimir Y.  
Padigaru, Muralidhara  
Patturajan, Meera  
Shenoy, Suresh G.  
Spytek, Kimberly A.

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His Lys Glu Leu Tyr Asp Trp Arg Leu Gly Pro Trp Asn Gln Cys Gln
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Pro Val Ile Ser Lys Ser Leu Glu Lys Pro Leu Glu Cys Ile Lys Gly
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Asp Ile Pro Ala Glu Asp Ile Ile Cys Glu Tyr Phe Glu Pro Lys Pro
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Glu	Trp	Ser	Val	Gly	Leu	Gly	Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	65	70	75	80
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65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
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Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
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His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
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Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
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 <211> 3447  
 <212> DNA  
 <213> human

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<210> 10  
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 <213> human

<400> 10

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Val Leu Leu Pro Cys Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
             35             40             45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
             50             55             60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
             65             70             75             80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
             85             90             95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
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Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
             115            120            125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
             130            135            140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
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Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
             165            170            175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
             180            185            190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
             195            200            205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
             210            215            220

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Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His  
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 Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile  
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 Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser  
 260 265 270  
 Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His  
 275 280 285  
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 Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala  
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 Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val  
 325 330 335  
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 340 345 350  
 Asn Pro Asp Glu Lys Thr Cys Thr Lys Ile Asp Tyr Cys Ala Ser Ser  
 355 360 365  
 Asn His Gly Cys Gln Tyr Glu Cys Val Asn Thr Asp Asp Ser Tyr Ser  
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 Cys His Cys Leu Lys Gly Phe Thr Leu Asn Pro Asp Lys Lys Thr Cys  
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 Arg Arg Ile Asn Tyr Cys Ala Leu Asn Lys Pro Gly Cys Glu His Glu  
 405 410 415  
 Cys Val Asn Met Glu Glu Ser Tyr Tyr Cys Arg Cys His Arg Gly Tyr  
 420 425 430  
 Thr Leu Asp Pro Asn Gly Lys Pro Cys Ser Arg Val Asp His Cys Ala  
 435 440 445  
 Gln Gln Asp His Gly Cys Glu Gln Leu Cys Leu Asn Thr Glu Asp Ser  
 450 455 460  
 Phe Val Cys Gln Cys Ser Glu Gly Phe Leu Ile Asn Glu Asp Leu Lys  
 465 470 475 480  
 Thr Cys Ser Arg Val Asp Tyr Cys Leu Leu Ser Asp His Gly Cys Glu  
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 Tyr Ser Cys Val Asn Met Asp Arg Ser Phe Ala Cys Gln Cys Pro Glu  
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 Gly His Val Leu Arg Ser Asp Gly Lys Thr Cys Ala Lys Leu Asp Ser  
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Cys Ala Leu Gly Asp His Gly Cys Glu His Ser Cys Val Ser Ser Glu  
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Asp Ser Phe Val Cys Gln Cys Phe Glu Gly Tyr Ile Leu Arg Glu Asp  
545 550 555 560

Gly Lys Thr Cys Arg Arg Lys Asp Val Cys Gln Ala Ile Asp His Gly  
565 570 575

Cys Glu His Ile Cys Val Asn Ser Asp Asp Ser Tyr Thr Cys Glu Cys  
580 585 590

Leu Glu Gly Phe Arg Leu Thr Glu Asp Gly Lys Arg Cys Arg Ile Ser  
595 600 605

Ser Gly Lys Asp Val Cys Lys Ser Thr His His Gly Cys Glu His Ile  
610 615 620

Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys Ser Glu Gly Phe  
625 630 635 640

Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys Thr Glu Gly Pro  
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Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser Leu Gly Glu Glu  
660 665 670

Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile Ile Asp Ser Leu  
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Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu Gln Tyr Ser Thr  
690 695 700

Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp  
705 710 715 720

Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly Lys Gly Ser Met  
725 730 735

Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser Phe Thr Gln Gly  
740 745 750

Glu Gly Ala Arg Pro Phe Ser Thr Arg Val Pro Arg Ala Ala Ile Val  
755 760 765

Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu Trp Ala Ser Lys  
770 775 780

Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly Val Gly Lys Ala  
785 790 795 800

Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro Thr Asn Lys His  
805 810 815

Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu Ile Ser Glu Lys  
820 825 830

Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser Asp Gly Arg Gln  
835 840 845

Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln Gln Pro Thr Glu  
850 855 860

Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu Ser Cys Ser Asn  
865 870 875 880

Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp Asn Leu Leu Arg  
885 890 895

Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser Gly Ser Pro Leu  
900 905 910

Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu Ile Met Phe Gln  
915 920 925

Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln Arg Leu Glu Glu  
930 935 940

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<211> 967

<212> DNA

<213> human

<400> 11

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967

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<211> 245

<212> PRT

<213> human

<400> 12

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                     20                      25                      30  
 Val Ser Ser Gly Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr  
                     35                      40                      45  
 Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu  
                     50                      55                      60  
 Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala  
                     65                      70                      75                      80  
 Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys  
                     85                      90                      95  
 Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn  
                     100                      105                      110  
 Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys  
                     115                      120                      125  
 Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr  
                     130                      135                      140  
 Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro  
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 Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu  
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 Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu  
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 Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Arg  
                     210                      215                      220  
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 Gly Leu Leu Thr Val  
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<212>	PRT
<213>	human

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Arg Ser Ala Gly Cys Trp Gly Ala Gly Glu Ala Pro Gly Ala Leu Ser  
35 40 45

Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr  
50 55 60

Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln  
65 70 75 80

Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly  
85 90 95

Lys Val Asp Pro Tyr Arg Ser Cys Gly Phe Ser Tyr Glu Gln Asp Pro  
100 105 110

Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val  
115 120 125

Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala  
130 135 140

Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val  
145 150 155 160









20					25					30					
Leu	Lys	Arg	Leu	Leu	Glu	Gln	Glu	Phe	Ala	Asp	Val	Ile	Val	Lys	Pro
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His	Asp	Pro	Ala	Thr	Val	Asp	Glu	Val	Leu	Arg	Leu	Leu	Asp	Glu	Asp
	50					55					60				
His	Thr	Gly	Thr	Val	Glu	Phe	Lys	Glu	Phe	Leu	Val	Leu	Val	Phe	Lys
65					70					75					80
Val	Ala	Gln	Ala	Cys	Phe	Lys	Thr	Leu	Ser	Glu	Ser	Ala	Glu	Gly	Ala
				85					90					95	
Cys	Gly	Ser	Gln	Glu	Ser	Gly	Ser	Leu	His	Ser	Gly	Ala	Ser	Gln	Glu
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Leu	Gly	Glu	Gly	Gln	Arg	Ser	Gly	Thr	Glu	Val	Gly	Arg	Ala	Gly	Lys
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Gly	Gln	His	Tyr	Glu	Gly	Ser	Ser	His	Arg	Gln	Ser	Gln	Gln	Gly	Ser
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Arg	Gly	Gln	Asn	Arg	Pro	Gly	Val	Gln	Thr	Gln	Gly	Gln	Ala	Thr	Gly
145					150					155					160
Ser	Ala	Trp	Val	Ser	Ser	Tyr	Asp	Arg	Gln	Ala	Glu	Ser	Gln	Ser	Gln
				165					170					175	
Glu	Arg	Ile	Ser	Pro	Gln	Ile	Gln	Leu	Ser	Gly	Gln	Thr	Glu	Gln	Thr
			180					185					190		
Gln	Lys	Ala	Gly	Glu	Gly	Lys	Arg	Asn	Gln	Thr	Thr	Glu	Met	Arg	Pro
		195					200					205			
Glu	Arg	Gln	Pro	Gln	Thr	Arg	Glu	Gln	Asp	Arg	Ala	His	Gln	Thr	Gly
	210					215					220				
Glu	Thr	Val	Thr	Gly	Ser	Gly	Thr	Gln	Thr	Gln	Ala	Gly	Ala	Thr	Gln
225					230					235					240
Thr	Val	Glu	Gln	Asp	Ser	Ser	His	Gln	Thr	Gly	Ser	Thr	Ser	Thr	Gln
				245					250					255	
Thr	Gln	Glu	Ser	Thr	Asn	Gly	Gln	Asn	Arg	Gly	Thr	Glu	Ile	His	Gly
			260					265					270		
Gln	Gly	Arg	Ser	Gln	Thr	Ser	Gln	Ala	Val	Thr	Gly	Gly	His	Thr	Gln
		275					280					285			
Ile	Gln	Ala	Gly	Ser	His	Thr	Glu	Thr	Val	Glu	Gln	Asp	Arg	Ser	Gln
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Thr	Val	Ser	His	Gly	Gly	Ala	Arg	Glu	Gln	Gly	Gln	Thr	Gln	Thr	Gln
305					310					315					320
Pro	Gly	Ser	Gly	Gln	Arg	Trp	Met	Gln	Val	Ser	Asn	Pro	Glu	Ala	Gly

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Glu	Thr	Val	Pro	Gly	Gly	Gln	Ala	Gln	Thr	Gly	Ala	Ser	Thr	Glu	Ser		
340								345					350				
Gly	Arg	Gln	Glu	Trp	Ser	Ser	Thr	His	Pro	Arg	Arg	Cys	Val	Thr	Glu		
355								360					365				
Gly	Gln	Gly	Asp	Arg	Gln	Pro	Thr	Val	Val	Gly	Glu	Glu	Trp	Val	Asp		
370								375					380				
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385								390					395				
His	Thr	Ser	Val	Ser	Ser	Ala	Gln	Gly	Gln	Asp	Ala	Ala	Gln	Ser	Glu		
405								410					415				
Glu	Lys	Arg	Gly	Ile	Thr	Ala	Arg	Glu	Leu	Tyr	Ser	Tyr	Leu	Arg	Ser		
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<210> 19
<211> 42
<212> DNA
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<210> 20
<211> 37
<212> DNA
<213> Artificial Sequence
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<220>  
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Oligonucleotide Primer

<400> 20  
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<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence:

1967-1968

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<210> 22
<211> 31
<212> DNA
<213> Artificial Sequence
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<400> 22  
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<210> 23
<211> 35
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide Primer

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Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met  
165 170 175

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Ala Asn Gln  
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Pro Ala Ala Asp Arg Gly Pro Gly His Ser Gln Glu Gln Glu Asn Ala  
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gccactgct ttgaaaaggc agcagcaaca gaactgaatt cctgcgtgag ggactcagcc 360  
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tccgggggcc ctgtgctgtg cctcgagcct gacggacact ggttccaggc tggcatcatc 780  
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[illegible]

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225					230					235					240
Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe
				245					250					255	
Ala	Ser	Ser	Cys	Ala	Gln	Glu	Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr
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Ala	Ala	His	Ser	Ser	Trp	Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe
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Leu	Ala	Gln	Ser	Pro	Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys
	290					295					300				
Val	Ala	Cys	Gly	Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro
305					310					315					320
Ser	Pro	Trp	Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala
				325					330					335	
Cys	Gly	Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His
			340					345					350		
Cys	Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly
		355					360					365			
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	Ala
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385					390					395					400
Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	Leu	Pro	Tyr
				405					410					415	
Ala	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	Val	Leu	Gly	Arg
			420					425				430			
Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	Thr	Val	Pro	Val	Thr
			435				440					445			
Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	His	Ala	Ala	Pro	Gly	Gly
	450					455					460				
Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	Val	Cys	Thr	Ser	Ala	Val	Gly
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Glu	Leu	Pro	Ser	Cys	Glu	Ala	Asn	Gln	Pro	Ala	Ala	Asp	Arg	Gly	Pro
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35 40 45  
Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp Leu Gln Ala  
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Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro Glu Thr Pro Glu  
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Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala

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Arg	Pro	Leu	Cys	Leu	Pro	Tyr	Ala	Asp	His	His	Leu	Pro	Asp	Gly	Glu
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Leu	His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met
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Pro	Ala	Ala	Asp	Arg	Gly	Pro	Gly	His	Ser	Gln	Glu	Gln	Glu	Asn	Ala
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Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala  
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 Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser  
 50 55 60  
 Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys  
 65 70 75 80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg  
 85 90 95  
 Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln  
 100 105 110  
 Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg  
 115 120 125  
 His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe  
 130 135 140  
 Gly Leu Leu Asp His Lys His Leu Asp His Glu Gly Gly Lys Pro Ala  
 145 150 155 160  
 Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His  
 165 170 175  
 Asn Val Ser Arg Leu His His Gly Gly Trp Thr Val Ile Gln Arg Arg  
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 His Asp Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala  
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 Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val  
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 His Ser Ile Met Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg  
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 Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly  
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 Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly  
 260 265 270  
 Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe  
 275 280 285  
 Ser Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala  
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 325 330 335  
 Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu  
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[illegible]

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51

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 Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala  
 145 150 155 160  
 Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His  
 165 170 175  
 Asn Val Ser Arg Leu His His Gly Gly Trp Thr Val Ile Gln Arg Arg  
 180 185 190  
 His Asp Gly Ser Met Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala  
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 Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val  
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 Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly  
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 Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe  
 275 280 285  
 Ser Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala  
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 Lys Ser Leu Ser Ala Pro Ser Val Ala Gln Arg Pro Asp His Val Pro  
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 Ser Pro Leu Thr Pro Ala Gly Gly Trp Trp Phe Gly Thr Cys Ser His  
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 Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr  
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 Ala Ser  
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$$\begin{aligned} & \left( \frac{\partial}{\partial t} + v^j \frac{\partial}{\partial x^j} - \Delta \right) u = f(x), \\ & u|_{t=0} = g(x). \end{aligned}$$

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<212> DNA  
<213> human

<400> 59

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```

<210> 60  
 <211> 1661  
 <212> DNA  
 <213> human

```

<400> 60
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tggctttgtt gcttggtctc agggagattc cgggggcct gtgctgtgcc tcgagcctga 360
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```





450 455 460

Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu  
 465 470 475 480

Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro  
 485 490 495

Gly Ser Cys Leu Ala  
 500

<210> 62  
 <211> 342  
 <212> DNA  
 <213> human

<400> 62

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<210> 63  
 <211> 1139  
 <212> DNA  
 <213> human

<400> 63

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<210> 64  
 <211> 768  
 <212> DNA  
 <213> human

<400> 64

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<210> 65

<211> 493

<212> PRT

<213> human

<400> 65

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```

```
Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
          20             25             30
```

```
Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
      35             40             45
```

```
Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn Thr Val Pro Gly
      50             55             60
```

```
Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln Gly Ala His Ile Cys
      65             70             75             80
```

```
Ser Gly Ser Leu Val Ala Asp Thr Trp Val Leu Thr Ala Ala His Cys
          85             90             95
```

```
Phe Glu Lys Ala Ala Ala Thr Glu Leu Asn Ser Trp Ser Val Val Leu
      100            105            110
```

```
Gly Ser Leu Gln Arg Glu Gly Leu Ser Pro Gly Ala Glu Glu Val Gly
      115            120            125
```

```
Val Ala Ala Leu Gln Leu Pro Arg Ala Tyr Asn His Tyr Ser Gln Gly
      130            135            140
```

```
Ser Asp Leu Ala Leu Leu Gln Leu Ala His Pro Thr Thr His Thr Pro
      145            150            155            160
```

```
Leu Cys Leu Pro Gln Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys
          165            170            175
```

```
Trp Ala Thr Gly Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu
```



485

490

<210> 66  
<211> 189  
<212> PRT  
<213> human

<400> 66

```

Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
  1          5          10          15

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
          20          25          30

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
          35          40          45

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
          50          55          60

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
          65          70          75          80

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
          85          90          95

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
          100          105          110

Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu
          115          120          125

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
          130          135          140

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
          145          150          155          160

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
          165          170          175

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu
          180          185

```

<210> 67  
<211> 186  
<212> DNA  
<213> human

<400> 67

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ggccaggtag acagaaccag cgagagacac cagggagctc agcagcatca ggacagaggc 180
ccagcg                                           186

```



*The following are the names of the persons who have been elected to the various offices of the Association:*

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<211>	180
<212>	DNA
<213>	human

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<210> 69  
<211> 157  
<212> DNA  
<213> human

```
<400> 69
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```

<210>	70
<211>	157
<212>	DNA
<213>	human

```

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```

<210>	71
<211>	842
<212>	DNA
<213>	human

<400> 71						
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			20					25					30		
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Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn
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Thr	Ala	Ala	His	Ser	Ser	Trp	Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala
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Phe	Leu	Ala	Gln	Ser	Pro	Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser
				85					90					95	
Cys	Val	Ala	Cys	Gly	Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala
			100					105					110		
Pro	Ser	Pro	Trp	Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu
		115					120					125			
Ala	Cys	Gly	Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala
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His	Cys	Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu
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35 40 45  
Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr  
50 55 60  
Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln  
65 70 75 80  
Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly  
85 90 95  
Lys Val Asp Pro Tyr Arg Ser Cys Gly Phe Ser Tyr Glu Gln Asp Pro  
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Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val  
115 120 125  
Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala  
130 135 140  
Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val  
145 150 155 160  
Ile Tyr Ser Val Arg Val Gly Ser Pro Trp Ile Asp Gln Met Thr Gln  
165 170 175  
Thr Ala Ser Asp Val Pro Val Leu Gln Val Ile Met His Ser Arg Tyr  
180 185 190  
Arg Ala Gln Arg Phe Trp Ser Trp Val Gly Gln Ala Asn Asp Ile Gly  
195 200 205  
Leu Leu Lys Leu Lys Gln Glu Leu Lys Tyr Ser Asn Tyr Val Arg Pro  
210 215 220











$$\sum_{i=1}^n \left( \frac{f_i'(t)}{f_i(t)} - \frac{f_i''(t)}{f_i(t)^2} \right) \leq \frac{f_1'(t)}{f_1(t)} - \frac{f_1''(t)}{f_1(t)^2} + \frac{f_2'(t)}{f_2(t)} - \frac{f_2''(t)}{f_2(t)^2} + \dots + \frac{f_n'(t)}{f_n(t)} - \frac{f_n''(t)}{f_n(t)^2}$$

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<212>	DNA
<213>	human

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tggtcccagg ccaacgaaag acggtgactc ttgggtccg 159
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<212>	DNA
<213>	human

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 <211> 406  
 <212> PRT  
 <213> human

<400> 88

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 50 55 60  
 Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys  
 65 70 75 80  
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 85 90 95  
 Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln  
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 Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg  
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 His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe  
 130 135 140  
 Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala  
 145 150 155 160  
 Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His  
 165 170 175  
 Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe  
 180 185 190  
 Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly  
 195 200 205  
 Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp  
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Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro  
 225 230 235 240

Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp  
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Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn Ser Arg  
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Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln  
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Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu  
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Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser  
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Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg  
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Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly  
 340 345 350

Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro  
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Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg  
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Gly Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met  
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Ala Ala Glu Ala Ala Ser  
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 <212> DNA  
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 gccccgccag gtcttccaga agattccctt cttaagcttc tgccgctgct gtgggatgga 180  
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<212> DNA  
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<210> 94  
<211> 1943



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Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg  
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Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln  
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Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg  
115 120 125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe  
130 135 140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala  
145 150 155 160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Pro His  
165 170 175

Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe  
180 185 190

Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly  
195 200 205

Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp  
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Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro  
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Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp  
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Leu Gly Leu Glu Lys Val His Ser Ile Met Gly Asp Arg Asn Ser Arg  
260 265 270

Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln  
275 280 285

Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Phe  
290 295 300

Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser  
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Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg  
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Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly  
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Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro  
355 360 365

Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg  
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Gly Arg Tyr Tyr Ser Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met  
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Ala Ala Glu Ala Ala Ser  
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accacttggg gccagccaga ctggcctcaa tggcggactc agtcacattg actgacgggg 1740
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cctggggaca caagcaggcg ccaatggtat ctgggcggcg tcacagagtt cttggaataa 1860
aagcaaccctc agaacactta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaa 1943

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<210> 98  
 <211> 406  
 <212> PRT  
 <213> human

<400> 98

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Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
  1              5              10              15

Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
      20              25              30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
      35              40              45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
      50              55              60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
      65              70              75              80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
      85              90              95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
      100             105             110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
      115             120             125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
      130             135             140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
      145             150             155             160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
      165             170             175

Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe
      180             185             190

Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly

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195 200 205

Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp  
210 215 220

Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro  
225 230 235 240

Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp  
245 250 255

Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn Ser Arg  
260 265 270

Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln  
275 280 285

Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu  
290 295 300

Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser  
305 310 315 320

Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg  
325 330 335

Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly  
340 345 350

Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro  
355 360 365

Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg  
370 375 380

Gly Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met  
385 390 395 400

Ala Ala Glu Ala Ala Ser  
405

<210> 99  
<211> 550  
<212> DNA  
<213> human

<400> 99  
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acaatgtcag ccgctgcac catggaggct ggacagtaat tcagaggcgc cacgatggct 180  
cagtggactt caaccggccc tgggaagcct acaaggcggg gtttggggat cccacggcg 240  
agttctggct gggctcggag aaggtgcata gcatcacggg ggaccgcaac agccgcctgg 300  
ccgtgcagct gcgggactgg gatggcaacg ccgagttgct gcagttctcc gtgcacctgg 360  
gtggcgagga caccgcctat agcctgcagc tactgcacc cgtggccggc cagctgggcg 420  
ccaccaccgt cccaccagc ggcctctccg taccctctc cacttgggac caggatcacg 480  
acctccgcag ggacaagaac tgcgccaaga gcctctctgg aggctggtgg tttggcacct 540

gagccattc

550

<210> 100  
<211> 523  
<212> DNA  
<213> human

<400> 100  
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agatgctgaa ttcgcagggt ctgcttctcc aggtgccgct gctgctgggc caccttgtgg 120  
aagagttgct ggatcctgct gttctgagcc ttgagttgtg tctgcaggct gtgaaggacc 180  
tcaggggtcca cccggctctc aggggctaac gggaggtcgg tggaccctc gggtccctga 240  
caggcggacc cgcacgcgct caggcgcgcg tccagcgcgc tcagctgact gcgggtgcgc 300  
tccgcgtgtt cgcgcagccc ctggccgagc tgcaggagtc cgtgcgccag gacattcacc 360  
tcgtcccagg acgcaaagcg cggcgacttg gactgcacgg gtccgccctg agcgctcagt 420  
agcacggcgg tggcgggcga gagcatcagg gctgccccgg ccgtcggagc accgctcacc 480  
ctcttaggta gcctgggagc ggggattcgg ggactcttcg ggg 523

<210> 101  
<211> 96  
<212> DNA  
<213> human

<400> 101  
ggtgcaggcg gctgacattg tgagccgggt caactggctg ggccatctcg ggcagcctct 60  
ttcttcgggc aggtttggcc acctcatggt ctaggt 96

<210> 102  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide Primer

<400> 102  
gacaggggca gtaatgcat ttgc

24

<210> 103  
<211> 177  
<212> DNA  
<213> human

<400> 103  
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tacacaccat ccccggcaga atagggtgct catcacccc aggagctgca tgcagccggc 120  
tgcaggccct agggcccagg aggttcacgg gactgtctg gagggagctg atgcctg 177

<210> 104  
<211> 63  
<212> DNA

[illegible]

<400> 104

ttggtgtgaa aatttccttt tttggggggc agcagttttc ctttttttaa acttaaataa 60  
att 63

<210> 105

<211> 1443

<212> DNA

<213> human

<400> 105

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agtgtgagga	ggcaaggagc	ccacatctgc	agcggctccc	tgggtggcaga	cacctgggtc	180
ctactgctg	ccactgctt	tgaaaaggca	gcagcaacag	aactgaattc	ctggtcagtg	240
gtcctgggtt	ctctgcagcg	tgagggaactc	agccctgggg	ccgaagaggt	gggggtggct	300
gccttcgagt	tgcccagggc	ctataaccac	tacagccagg	gtcagacct	ggccttgctg	360
cagctcgccc	accccacgac	ccacacacc	ctctgcttgc	cccagcccg	ccatcgcttc	420
cccttggag	cctcctgtg	ggccactggc	tgggactcagg	acaccagtga	tgctctcttg	480
accctacgca	atctgcgcct	gcgtctcatc	agtcgcccc	catgtaacta	tatctacaac	540
cagctgcacc	agcgacacct	gtccaaccgc	gcccggcctg	ggatgctatg	tgggggcccc	600
cagcctgggg	tgcaggggcc	ctgtcaggga	gattccgggg	gccttgtgct	gtgcctcgag	660
cctgacggac	actgggttca	ggctggcatc	atcagctttg	catcaagctg	tgcccaggag	720
gacgtcctg	tgtgtctgac	caacacagct	gctcacagtt	cctggctgca	ggctcgagtt	780
cagggggcag	ctttcctggc	ccagagccca	gagaccccg	agatgagtga	tgaggacagc	840
tgttagctc	gtggatcctt	gaggacagca	ggtccccagg	caggagcacc	ctccccatgg	900
ccctgggagg	ccaggctgat	gcaccaggga	cagctggcct	gtggcggagc	cctgggtgtca	960
gaggaggcgg	tgctaactgc	tgcccaactgc	ttcattgggc	gccaggcccc	agaggaatgg	1020
agcgtagggc	tggggaccag	accggaggag	tggggcctga	agcagctcat	cctgcatgga	1080
gcctacacc	accctgaggg	gggctacgac	atggccctcc	tgctgtggc	ccagcctgtg	1140
acactgggag	ccagcctgcg	gcccctctgc	ctgccctatc	ctgaccacca	cctgcctgat	1200
ggggagcgtg	gctgggttct	gggacggggc	cgcccaggag	caggcatcag	ctccctccag	1260
acagtgcccg	tgacctctct	ggggcctagg	gcctgcagcc	ggctgcatgc	agctcctggg	1320
ggtgatggca	gcctatttct	gccggggatg	gtgtgtacca	gtgctgtggg	tgagctgcc	1380
agctgtgagg	gcctgtctgg	ggcaccactg	gtgcatgagg	tgaggggcac	atggttctctg	1440
gcc						1443

<210> 106

<211> 186

<212> DNA

<213> human

<400> 106

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ctggcctgga	tccgtgtctt	cgtgctctat	gatttctgca	ttgtttgtat	caccacctat	120
gctatcaacg	tgagcctgat	gtggctcagt	ttccggaagg	tccaagaacc	ccagggcaag	180
gctaag						186

<210> 107

<211> 599

<212> DNA

<213> human



<211> 666  
<212> DNA  
<213> human

<400> 110  
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gccctggtgt cagaggaggc ggtgctaact gctgccact gcttcattgg gcgccaggcc 120  
ccagaggaat ggagcgtagg gctggggacc agaccggagg agtggggcct gaagcagctc 180  
atcctgcatg gagcctacac ccaccctgag gggggctacg acatggccct cctgctgctg 240  
gcccagcctg tgacactggg agccagcctg cggccctct gctgccta tgctgaccac 300  
cacctgcctg atggggagcg tggctgggtt ctgggacggg cccgcccagg agcaggcatc 360  
agctccctcc agacagtgcc cgtgaccctc ctggggccta gggcctgcag cgggctgcat 420  
gcagctcctg ggggtgatgg cagccctatt ctgccgggga tgggtgtgtac cagtgtgtgtg 480  
ggtgagctgc ccagctgtga gggcctgtct ggggcaccac tgggtgcatga ggtgaggggc 540  
acatggttcc tggccgggct gcacagcttc ggagatgctt gccaaggccc cgccaggccg 600  
gcggtcttca ccgcgctccc tgcctatgag gactgggtca gcagtttggga ctggcaggtc 660  
tacttc 666

<210> 111  
<211> 242  
<212> PRT  
<213> human

<400> 111  
Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu Met  
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His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu Ala  
20 25 30  
Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu Glu  
35 40 45  
Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln  
50 55 60  
Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met  
65 70 75 80  
Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg  
85 90 95  
Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg  
100 105 110  
Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu  
115 120 125  
Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu  
130 135 140  
His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met Val  
145 150 155 160  
Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser Gly  
165 170 175

Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly Leu  
180 185 190

His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val Phe  
195 200 205

Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp Gln  
210 215 220

Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser Cys  
225 230 235 240

Leu Ala

<210> 112  
<211> 242  
<212> PRT  
<213> human

<400> 112  
Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu Met  
1 5 10 15

His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu Ala  
20 25 30

Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu Glu  
35 40 45

Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln  
50 55 60

Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met  
65 70 75 80

Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg  
85 90 95

Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu Arg  
100 105 110

Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu  
115 120 125

Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu  
130 135 140

His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met Val  
145 150 155 160

Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser Gly  
165 170 175

Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly Leu







ccagtgcctgt gggtagctg cccagctgtg agggcctgtc tggggcacca ctggtgc 1017

<210> 118  
<211> 203  
<212> PRT  
<213> human

<400> 118

Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln Gly Ala His  
1 5 10 15

Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val Leu Thr Ala Ala  
20 25 30

His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu Asn Ser Trp Ser Val  
35 40 45

Val Leu Gly Ser Leu Gln Arg Glu Gly Leu Ser Pro Gly Ala Glu Glu  
50 55 60

Val Gly Val Ala Ala Leu Gln Leu Pro Arg Ala Tyr Asn His Tyr Ser  
65 70 75 80

Gln Gly Ser Asp Leu Ala Leu Leu Gln Leu Ala His Pro Thr Thr His  
85 90 95

Thr Pro Leu Cys Leu Pro Gln Pro Ala His Arg Phe Pro Phe Gly Ala  
100 105 110

Ser Cys Trp Ala Thr Gly Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly  
115 120 125

Thr Leu Arg Asn Leu Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn  
130 135 140

Cys Ile Tyr Asn Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg  
145 150 155 160

Pro Gly Met Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys  
165 170 175

Gln Gly Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His  
180 185 190

Trp Val Gln Ala Gly Ile Ile Ser Phe Ala Ser  
195 200

<210> 119  
<211> 90  
<212> PRT  
<213> human

<400> 119

Ser Pro Ile Leu Pro Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu  
1 5 10 15

Pro Ser Cys Glu Gly Leu Ser Gly Ala Pro Leu Val His Glu Val Arg  
20 25 30  
Gly Thr Trp Phe Leu Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln  
35 40 45  
Gly Pro Ala Arg Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp  
50 55 60  
Trp Val Ser Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu  
65 70 75 80  
Pro Glu Ala Glu Pro Gly Ser Cys Leu Ala  
85 90

<210> 120  
<211> 90  
<212> PRT  
<213> human

<400> 120  
Ser Pro Ile Leu Pro Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu  
1 5 10 15  
Pro Ser Cys Glu Gly Leu Ser Gly Ala Pro Leu Val His Glu Val Arg  
20 25 30  
Gly Thr Trp Phe Leu Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln  
35 40 45  
Gly Pro Ala Arg Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp  
50 55 60  
Trp Val Ser Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu  
65 70 75 80  
Pro Glu Ala Glu Pro Gly Ser Cys Leu Ala  
85 90

<210> 121  
<211> 177  
<212> DNA  
<213> human

<400> 121  
aggtaagggtg tggggggcctg ggggtcacct cacagctggg cagctcaccc acagcactgg 60  
tacacaccat ccccggcaga atagggctgc catcaccccc aggagctgca tgcagccggc 120  
tgcaggccct agggcccagg agggtcacgg gcactgtctg gagggagctg atgcctg 177

<210> 122  
<211> 571  
<212> PRT  
<213> human



[illegible]

Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala  
305 310 315 320

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu  
325 330 335

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu  
340 345 350

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu  
355 360 365

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys  
370 375 380

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp  
385 390 395 400

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu  
405 410 415

Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu  
420 425 430

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser  
435 440 445

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg  
450 455 460

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met  
465 470 475 480

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser  
485 490 495

Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly  
500 505 510

Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val  
515 520 525

Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp  
530 535 540

Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser  
545 550 555 560

Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser Cys  
565 570

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<210> 123
<211> 267
<212> PRT
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<213> human

<400> 123

Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala  
 1 5 10 15  
 Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu  
 20 25 30  
 Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu  
 35 40 45  
 Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu  
 50 55 60  
 Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys  
 65 70 75 80  
 Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp  
 85 90 95  
 Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu  
 100 105 110  
 Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu  
 115 120 125  
 Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser  
 130 135 140  
 Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg  
 145 150 155 160  
 Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met  
 165 170 175  
 Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser  
 180 185 190  
 Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly  
 195 200 205  
 Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val  
 210 215 220  
 Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp  
 225 230 235 240  
 Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser  
 245 250 255  
 Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser Cys  
 260 265

<210> 124

<211> 314

$$\frac{d}{dt} \left( \frac{1}{2} m v^2 + U \right) = - \nabla \cdot (\mathbf{v} p) + \nabla \cdot (\mathbf{v} \cdot \boldsymbol{\tau}) + \nabla \cdot (\mathbf{v} \cdot \mathbf{g}) + \nabla \cdot (\mathbf{v} \cdot \mathbf{f})$$

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala  
1 5 10 15

Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala  
35 40 45

Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser  
50 55 60

His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala  
65 70 75 80

Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp  
85 90 95

Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	Met	Pro	Ser	Phe	Trp	Ser	Leu
			100					105					110		

Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro  
115 120 125

Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser  
130 135 140

Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala  
145 150 155 160

Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp  
165 170 175

Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln  
180 185 190

Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe  
195 200 205

Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala  
210 215 220

Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
225 230 235 240

Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val  
245 250 255

Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr  
260 265 270

Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser  
275 280 285

Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu  
 290 295 300

Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310

<210> 125  
 <211> 343  
 <212> PRT  
 <213> human

<400> 125  
 Met Ala Gln Lys Gly Val Leu Gly Pro Gly Gln Leu Gly Ala Val Ala  
 1 5 10 15

Ile Leu Leu Tyr Leu Gly Leu Leu Arg Ser Gly Thr Gly Ala Glu Gly  
 20 25 30

Ala Glu Ala Pro Cys Gly Val Ala Pro Gln Ala Arg Ile Thr Gly Gly  
 35 40 45

Ser Ser Ala Val Ala Gly Gln Trp Pro Trp Gln Val Ser Ile Thr Tyr  
 50 55 60

Glu Gly Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln Trp Val  
 65 70 75 80

Leu Ser Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu Ala Tyr  
 85 90 95

Glu Val Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu Asp Ala  
 100 105 110

Lys Val Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr Leu Gln  
 115 120 125

Glu Gly Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg Pro Ile  
 130 135 140

Thr Phe Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala Asn Ala  
 145 150 155 160

Ser Phe Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly His Val  
 165 170 175

Ala Pro Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln Leu Glu  
 180 185 190

Val Pro Leu Ile Ser Arg Glu Thr Cys Asn Cys Leu Tyr Asn Ile Asp  
 195 200 205

Ala Lys Pro Glu Glu Pro His Phe Val Gln Glu Asp Met Val Cys Ala  
 210 215 220

Gly Tyr Val Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly





<400> 126

Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
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 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40 45  
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
 50 55 60  
 Xaa Xaa Xaa Xaa Xaa  
 65

<210> 127

<211> 245

<212> DNA

<213> human

<400> 127

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 gcccgcagcag gtcttccaga agattccctt cttaagcttc tgccgctgct gtgggatgga 180  
 gcggaagtac tggccgttga gggttgaatg gctgcagggtg ccaaaccacc agcctccaga 240  
 gaggc 245

<210> 128

<211> 245

<212> DNA

<213> human

<400> 128

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<211> 91

<212> DNA

<213> human

<400> 129

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<210> 130

<211> 413

<212> DNA

[illegible]

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 $\langle 211 \rangle$  401

<212> DNA

<213> human

<400> 131

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ggagaagggt	acggagagggc	cgctgggtgg	gacggtgggt	gcgccagct	ggccggccac	300
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<212> DNA

<213> human

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